RECEIVED

JAN 1 2 2004

ENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 01/12/2004

PATENT APPLICATION: US/10/650,369A

TIME: 10:36:11

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt Output Set: N:\CRF4\01092004\J650369A.raw

1 <110> APPLICANT: Potter, Andrew A. 2 Perez-Casal, Jose Fontaine, Michael 4 <120> TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN AGAINST STREPTOCOCCUS INFECTION 6 <130> FILE REFERENCE: 9000-0057 7 <140> CURRENT APPLICATION NUMBER: 10/650,369A 8 <141> CURRENT FILING DATE: 2003-08-27 9 <150> PRIOR APPLICATION NUMBER: US/09/878,766A 10 <151> PRIOR FILING DATE: 2001-09-10 11 <160> NUMBER OF SEQ ID NOS: 22 12 <170> SOFTWARE: PatentIn Ver. 2.0 14 <210> SEQ ID NO: 1 15 <211> LENGTH: 37 16 <212> TYPE: DNA 17 <213> ORGANISM: Artificial Sequence 18 <220> FEATURE: 19 <223> OTHER INFORMATION: Description of Artificial Sequence: primer gapC1 20 <400> SEQUENCE: 1 37 qqcqqcqgca tatggtagtt aaagttggta ttaacgg 23 <210> SEQ ID NO: 2 24 <211> LENGTH: 35 25 <212> TYPE: DNA 26 <213> ORGANISM: Artificial Sequence 27 <220> FEATURE: 28 <223> OTHER INFORMATION: Description of Artificial Sequence: primer gapClr 29 <400> SEQUENCE: 2 35 gcggatcctt atttagcgat ttttgcaaag tactc 32 <210> SEQ ID NO: 3 33 <211> LENGTH: 32 34 <212> TYPE: DNA 35 <213> ORGANISM: Artificial Sequence 36 <220> FEATURE: 37 <223> OTHER INFORMATION: Description of Artificial Sequence: primer gap-1 38 <400> SEQUENCE: 3 32 aaaaaaggat ccggtatggt agttaaagtt gg 41 <210> SEQ ID NO: 4 42 <211> LENGTH: 39 43 <212> TYPE: DNA 44 <213> ORGANISM: Artificial Sequence 45 <220> FEATURE: 46 <223> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-2

47 <400> SEQUENCE: 4

RAW SEQUENCE LISTING

DATE: 01/12/2004 PATENT APPLICATION: US/10/650,369A TIME: 10:36:11

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt
Output Set: N:\CRF4\01092004\J650369A.raw

48		aaaaaaccat ggttactcga gtgcttccag aacgatttc 39
		SEQ ID NO: 5
51	<211>	LENGTH: 31
		TYPE: DNA
53	<213>	ORGANISM: Artificial Sequence
		FEATURE:
55	<223>	OTHER INFORMATION: Description of Artificial Sequence: primer Gap-3
56	<400>	SEQUENCE: 5
57		aaaaaactcg agggtactgt agaagttaaa g 31
59	<210>	SEQ ID NO: 6
60	<211>	LENGTH: 45
61	<212>	TYPE: DNA
62	<213>	ORGANISM: Artificial Sequence
		FEATURE:
		OTHER INFORMATION: Description of Artificial Sequence: primer Gap-4
		SEQUENCE: 6
66		aaaaaaccat ggttaatcga tttcaagaac gatttcaaca ccgtc 45
	<210>	SEQ ID NO: 7
		LENGTH: 34
		TYPE: DNA
		ORGANISM: Artificial Sequence
		FEATURE:
		OTHER INFORMATION: Description of Artificial Sequence: primer Gap-5
		SEQUENCE: 7
75	(400)	aaaaaaatcg atggtactgt tgaagttaaa gaag 34
	<210S	SEQ ID NO: 8
		LENGTH: 45
		TYPE: DNA
		ORGANISM: Artificial Sequence
		FEATURE:
		OTHER INFORMATION: Description of Artificial Sequence: primer Gap-6
		SEQUENCE: 8
	<400>	
84	<010×	addadood ggooddood oogooddaag aarganii aagaa
		SEQ ID NO: 9
_		LENGTH: 35
		TYPE: DNA
		ORGANISM: Artificial Sequence
		FEATURE:
		OTHER INFORMATION: Description of Artificial Sequence: primer Gap-7
	<400>	SEQUENCE: 9
93		aaaaaaacta gtttctttgc taaaaaagaa gctgc . 35
		SEQ ID NO: 10
		LENGTH: 42
		TYPE: DNA
		ORGANISM: Artificial Sequence
		FEATURE:
		> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-8
		> SEQUENCE: 10
102	2	aaaaaaccat ggctattatt tagcgatttt tgcaaaatac tc 42

RAW SEQUENCE LISTING DATE: 01/12/2004 PATENT APPLICATION: US/10/650,369A TIME: 10:36:11

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt
Output Set: N:\CRF4\01092004\J650369A.raw

105 106	<210><211><212><212><213>	LENO TYPI	GTH: E: Di	101: NA	1	- 000	ccus	dvse	galad	ctiae	.							
	<220>				c.cp.			~			_							
	<221>				os													
110	<222>	LOCA	OITA	N: (1	1)	(101	l)											
	<400>																	• •
112									aac									48
113			Val	Val	Lys	Val	GТУ	Ile	Asn	GLY		GLY	Arg	тте	GTÀ		Leu	
114		1	++~	~~t	~~+	5	000	22+	gtt	~~~	10	~++	~~~	at a	act	15 cat	atc	96
115 116									Val									50
117		Ата	FILE	Arg	20	116	GLII	ASII	Val	25	ОТУ	VUL	Olu	V 4 1	30	1119	110	
118		aac	gac	ctt		gat	сса	aac	atg		qca	cac	ttq	tta		tac	gat	144
119									Met									
120			-	35		-			40					45	_	_	_	
121		aca	act	caa	gga	cgt	ttt	gac	gga	act	gtt	gaa	gtt	aaa	gaa	ggt	gga	192
122		Thr	Thr	Gln	Gly	Arg	Phe		Gly	Thr	Val	Glu		Lys	Glu	Gly	Gly	
123			50					55					60					0.40
124									atc									240
125			Glu	Val	Asn	GLy		Phe	Ile	Lys	Val		Ala	GIU	Arg	Asp	80	
126		65	222	2+0	~~~	+~~	70	20+	gac	aat	a++	75	a+c	att	cta	ma a		288
127 128									Asp									200
129		GIU	HSII	116	изр	85	п.ε.α	1111	7150	O _T y	90	OLU	110	• • • •	200	95		
130		act	aat	ttc	ttt		aaa	aaa	ġaa	act		qaa	aaa	cac	tta		gct	336
131									Ğlu									
132			-		100		-	_		105					110			
133									atc									384
134		Asn	Gly		_	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly		Asn	Asp	Val	
135				115					120					125				420
136									aac									432
137 138		гàг	130	vaı	vaı	Pne	ASII	135	Asn	птѕ	Asp	116	140	ASP	сту	1111	Giu	
139		aca	_	atc	tca	aat	act		tgt	act	aca	aac		tta	act.	cct	atg	480
140									Cys									
141		145				1	150		- 1 -			155	2				160	
142			aaa	gct	ctt	cac	gat	gca	ttt	ggt	atc	caa	aaa	ġgt	ctt	atg	act	528
143									Phe									
144						165					170					175		
145		aca	atc	cac	gct	tat	act	ggt	gac	caa	atg	atc	ctt	gac	gga	cca	cac	576
146		Thr	Ile	His		Tyr	Thr	Gly	Asp		Met	Ile	Leu	Asp		Pro	His	
147					180					185					190			624
148									gct									624
149		Arg	етλ		Asp	ьeu	Arg	Arg	Ala 200	Arg	ATG	сту	HTG	205	ASII	тте	val	
150 151		cct	220	195	act	aat	act	act	aaa	act	atc	aat	ctt		atc	cca	gaa	672
151		Pro	Asn	Ser	Thr	Glv	Ala	Ala	Lys	Ala	Tle	G] v	Leu	Val	Ile	Pro	Glu	J. 2
102		110	11611	Der	1111	ULY.	1 1.L. U		273		220	1						

RAW SEQUENCE LISTING DATE: 01/12/2004 PATENT APPLICATION: US/10/650,369A TIME: 10:36:11

Input Set: N:\Crf3\RULE60\10650369A.RAW.txt
Output Set: N:\CRF4\01092004\J650369A.raw

153	210	1				215					220					
154	ttg aat	ggt	aaa	ctt	gat	ggt	gct	gca	caa	cgt	gtt	cct	gtt	cca	act	720
155	Leu Asr															
156	225	-	.		230	-				235					240	
157	gġa tca	αta	act	gag	tta	att	σta	act	ctt	gat	aaa	aac	qtt	tct	qtt	768
158	Gly Ser															
159	01, 001			245					250					255		
160	gac gaa	atc	aac		act	ato	aaa	act		tca	aac	gac	aαt.		aat.	816
161	Asp Glu	Tle	Acn	Δla	Δla	Met	Lvs	Δla	Ala	Ser	Asn	Asp	Ser	Phe	Glv	
162	ASP GIO	1 116	260	лта	ALG	Mec	БуЗ	265	1114	001	71011	1100	270			
	tac act	. ~~~			a++	a++	t ct		ast.	atc	at a	aac		tca	tac	864
163	Tyr Thi	. gaa	yat	Dwa	TIA	yet	Cox	Cor	yar Nan	TIA	Val	Glu	Val	Sar	Tur	001
164	Tyr Ini			PIO	тте.	vai	280	Ser	АЗР	116	vaı	285	Val	Ser	ıyı	
165		275									~+~		~++	~~~	~~~	912
166	ggt tca															912
167	Gly Ser		Phe	Asp	Ата		GIn	Thr	гàг	vaı		GIU	vaı	Asp	GTÀ	
168	290					295					300					0.00
169	tca caa															960
170	Ser Glr	ı Leu	Val.	Lys		Val	Ser	Trp	Tyr		Asn	GLu	Met	Ser		
171	305				310	•				315					320	
172	act gct															1008
173	Thr Ala	Gln	Leu		_	Thr	Leu	Glu	Tyr	Phe	Ala	Lys	Ile		Lys	
174				325					330					335		
175	taa															1011
177 -010	CEO ID	NO.	1 2													
177 <210>	2FO ID	NO:	12													
177 <210>	-		12													
	LENGTH:	336	12													
178 <211> 179 <212>	LENGTH:	336 PRT		toco	ccus	dys	gala	ctiae	e							
178 <211>	LENGTH: TYPE: I	336 PRT SM: S	trep	toco	ccus	dys	gala	ctia	ę			•			•	
178 <211> 179 <212> 180 <213>	LENGTH: TYPE: I	336 PRT SM: S CE: 1	trep [.] 2							Gly	Arg	Ile	Gly	Arg	Leu	
178 <211> 179 <212> 180 <213> 181 <400> 182	LENGTH: TYPE: I ORGANIS SEQUENCE	336 PRT SM: S CE: 1	trep [.] 2							Gly	Arg	Ile	Gly	Arg 15	Leu	
178 <211> 179 <212> 180 <213> 181 <400> 182 183	LENGTH: TYPE: I ORGANIS SEQUENC Met Val	336 PRT SM: S CE: 1: Val	trep [.] 2 Lys	Val 5	Gly	Ile	Asn	Gly	Phe					15		
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184	LENGTH: TYPE: I ORGANIS SEQUENCE Met Val	336 PRT SM: S CE: 1: Val	trep [.] 2 Lys	Val 5	Gly	Ile	Asn	Gly	Phe					15		
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe	336 PRT SM: S CE: 1 Val	trep [.] 2 Lys Arg 20	Val 5 Ile	Gly Gln	Ile Asn	Asn Val	Gly Glu 25	Phe 10 Gly	Val	Glu	Val	Thr 30	15 Arg	Ile	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186	LENGTH: TYPE: I ORGANIS SEQUENC Met Val	336 PRT SM: S CE: 1 Val	trep [.] 2 Lys Arg 20	Val 5 Ile	Gly Gln	Ile Asn	Asn Val	Gly Glu 25	Phe 10 Gly	Val	Glu	Val	Thr 30	15 Arg	Ile	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp	336 PRT SM: S CE: 1 Val PARG Arg	trep 2 Lys Arg 20 Thr	Val 5 Ile Asp	Gly Gln Pro	Ile Asn Asn	Asn Val Met 40	Gly Glu 25 Leu	Phe 10 Gly Ala	Val His	Glu Leu	Val Leu 45	Thr 30 Lys	15 Arg Tyr	Ile Asp	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe	336 PRT SM: S SE: 1 Val Arg Leu 35 Gln	trep 2 Lys Arg 20 Thr	Val 5 Ile Asp	Gly Gln Pro	Ile Asn Asn	Asn Val Met 40	Gly Glu 25 Leu	Phe 10 Gly Ala	Val His	Glu Leu	Val Leu 45	Thr 30 Lys	15 Arg Tyr	Ile Asp	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp	336 PRT SM: S SE: 1 Val Arg Leu 35 Gln	trep 2 Lys Arg 20 Thr	Val 5 Ile Asp	Gly Gln Pro	Ile Asn Asn Asp	Asn Val Met 40 Gly	Gly Glu 25 Leu Thr	Phe 10 Gly Ala Val	Val His Glu	Glu Leu Val 60	Val Leu 45 Lys	Thr 30 Lys Glu	15 Arg Tyr Gly	Ile Asp Gly	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu	336 PRT SM: S SE: 1 Val Arg Leu 35 Gln	trep 2 Lys Arg 20 Thr	Val 5 Ile Asp	Gly Gln Pro	Ile Asn Asn Asp	Asn Val Met 40 Gly	Gly Glu 25 Leu Thr	Phe 10 Gly Ala Val	Val His Glu	Glu Leu Val 60	Val Leu 45 Lys	Thr 30 Lys Glu	15 Arg Tyr Gly	Ile Asp Gly	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191	LENGTH: TYPE: IORGANIS SEQUENCE Met Val Ala Phe Asn Asp Thr Thr 50 Phe Glu 65	336 PRT SM: S CE: 1. Val Arg D Leu 35 Gln	trep 2 Lys Arg 20 Thr Gly Asn	Val 5 Ile Asp Arg	Gly Gln Pro Phe Asn 70	Ile Asn Asn Asp 55 Phe	Asn Val Met 40 Gly Ile	Gly Glu 25 Leu Thr	Phe 10 Gly Ala Val	Val His Glu Ser 75	Glu Leu Val 60 Ala	Val Leu 45 Lys Glu	Thr 30 Lys Glu Arg	15 Arg Tyr Gly Asp	Ile Asp Gly Pro 80	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu	336 PRT SM: S CE: 1. Val Arg D Leu 35 Gln	trep 2 Lys Arg 20 Thr Gly Asn	Val 5 Ile Asp Arg Gly Trp	Gly Gln Pro Phe Asn 70	Ile Asn Asn Asp 55 Phe	Asn Val Met 40 Gly Ile	Gly Glu 25 Leu Thr	Phe 10 Gly Ala Val Val	Val His Glu Ser 75	Glu Leu Val 60 Ala	Val Leu 45 Lys Glu	Thr 30 Lys Glu Arg	15 Arg Tyr Gly Asp	Ile Asp Gly Pro 80	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu 65 Glu Asn	336 PRT SM: S CE: 1 Val Arg Leu 35 Gln Val	trep 2 Lys Arg 20 Thr Gly Asn	Val 5 11e Asp Arg Gly Trp 85	Gly Gln Pro Phe Asn 70 Ala	Ile Asn Asn Asp 55 Phe Thr	Asn Val Met 40 Gly Ile Asp	Glu 25 Leu Thr Lys Gly	Phe 10 Gly Ala Val Val	Val His Glu Ser 75 Glu	Glu Leu Val 60 Ala	Val Leu 45 Lys Glu Val	Thr 30 Lys Glu Arg Leu	15 Arg Tyr Gly Asp Glu 95	Ile Asp Gly Pro 80 Ala	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194	LENGTH: TYPE: IORGANIS SEQUENCE Met Val Ala Phe Asn Asp Thr Thr 50 Phe Glu 65	336 PRT SM: S CE: 1 Val Arg Leu 35 Gln Val	trep 2 Lys Arg 20 Thr Gly Asn Asp	Val 5 11e Asp Arg Gly Trp 85	Gly Gln Pro Phe Asn 70 Ala	Ile Asn Asn Asp 55 Phe Thr	Asn Val Met 40 Gly Ile Asp	Glu 25 Leu Thr Lys Gly	Phe 10 Gly Ala Val Val	Val His Glu Ser 75 Glu	Glu Leu Val 60 Ala	Val Leu 45 Lys Glu Val	Thr 30 Lys Glu Arg Leu	15 Arg Tyr Gly Asp Glu 95	Ile Asp Gly Pro 80 Ala	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu 65 Glu Asr	336 PRT SM: S E: 1 Val Arg Leu 35 Gln Val Val	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe	Val 5 Ile Asp Arg Gly Trp 85 Ala	Gly Gln Pro Phe Asn 70 Ala Lys	Ile Asn Asn Asp 55 Phe Thr	Asn Val Met 40 Gly Ile Asp Glu	Gly Glu 25 Leu Thr Lys Gly Ala 105	Phe 10 Gly Ala Val Val Val 90 Ala	Val His Glu Ser 75 Glu Glu	Glu Leu Val 60 Ala Ile Lys	Val Leu 45 Lys Glu Val	Thr 30 Lys Glu Arg Leu Leu 110	15 Arg Tyr Gly Asp Glu 95 His	Ile Asp Gly Pro 80 Ala Ala	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu 65 Glu Asn	336 PRT SM: S E: 1 Val Arg Leu 35 Gln Val Ile Phe Ala	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe 100 Lys	Val 5 Ile Asp Arg Gly Trp 85 Ala	Gly Gln Pro Phe Asn 70 Ala Lys	Ile Asn Asn Asp 55 Phe Thr	Asn Val Met 40 Gly Ile Asp Glu Ile	Gly Glu 25 Leu Thr Lys Gly Ala 105	Phe 10 Gly Ala Val Val Val 90 Ala	Val His Glu Ser 75 Glu Glu	Glu Leu Val 60 Ala Ile Lys	Val Leu 45 Lys Glu Val His	Thr 30 Lys Glu Arg Leu Leu 110	15 Arg Tyr Gly Asp Glu 95 His	Ile Asp Gly Pro 80 Ala Ala	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thi 50 Phe Glu 65 Glu Asn Thr Gly Asn Gly	336 PRT SM: S CE: 1 Val Arg Leu 35 Gln Val I Val	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe 100 Lys	Val 5 Ile Asp Arg Gly Trp 85 Ala	Gly Gln Pro Phe Asn 70 Ala Lys Val	Ile Asn Asn Asp 55 Phe Thr Lys Val	Asn Val Met 40 Gly Ile Asp Glu Ile 120	Gly Glu 25 Leu Thr Lys Gly Ala 105 Thr	Phe 10 Gly Ala Val Val Val Ala Ala	Val His Glu Ser 75 Glu Glu Pro	Glu Leu Val 60 Ala Ile Lys Gly	Val Leu 45 Lys Glu Val His Gly 125	Thr 30 Lys Glu Arg Leu 110 Asn	15 Arg Tyr Gly Asp Glu 95 His	Ile Asp Gly Pro 80 Ala Ala Val	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu 65 Glu Asr Thr Gly Asn Gly Lys Thr	336 PRT SM: S CE: 1 Val Arg Leu 35 Gln Val 1 Val 1 Phe 7 Ala 115 Val	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe 100 Lys	Val 5 Ile Asp Arg Gly Trp 85 Ala	Gly Gln Pro Phe Asn 70 Ala Lys Val	Ile Asn Asn Asp 55 Phe Thr Lys Val Thr	Asn Val Met 40 Gly Ile Asp Glu Ile 120	Gly Glu 25 Leu Thr Lys Gly Ala 105 Thr	Phe 10 Gly Ala Val Val Val Ala Ala	Val His Glu Ser 75 Glu Glu Pro	Glu Leu Val 60 Ala Ile Lys Gly Leu	Val Leu 45 Lys Glu Val His Gly 125	Thr 30 Lys Glu Arg Leu 110 Asn	15 Arg Tyr Gly Asp Glu 95 His	Ile Asp Gly Pro 80 Ala Ala Val	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thi 50 Phe Glu 65 Glu Asn Thr Gly Asn Gly Lys Thi 130	336 PRT SM: S CE: 1 Val Arg Leu 35 Gln Val 1 Val 1 Phe 7 Ala 115 Val	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe 100 Lys	Val 5 Ile Asp Arg Gly Trp 85 Ala Lys	Gly Gln Pro Phe Asn 70 Ala Lys Val Asn	Ile Asn Asn Asp 55 Phe Thr Lys Val Thr 135	Asn Val Met 40 Gly Ile Asp Glu Ile 120 Asn	Gly Glu 25 Leu Thr Lys Gly Ala 105 Thr	Phe 10 Gly Ala Val Val 90 Ala Ala Asp	Val His Glu Ser 75 Glu Glu Pro Ile	Glu Leu Val 60 Ala Ile Lys Gly Leu 140	Val Leu 45 Lys Glu Val His Gly 125 Asp	Thr 30 Lys Glu Arg Leu 110 Asn	15 Arg Tyr Gly Asp Glu 95 His Asp	Ile Asp Gly Pro 80 Ala Ala Val Glu	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thr 50 Phe Glu 65 Glu Asr Thr Gly Asn Gly Lys Thr 130 Thr Val	336 PRT SM: S CE: 1 Val Arg Leu 35 Gln Val 1 Val 1 Phe 7 Ala 115 Val	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe 100 Lys	Val 5 Ile Asp Arg Gly Trp 85 Ala Lys	Gly Gln Pro Phe Asn 70 Ala Lys Val Asn Ala	Ile Asn Asn Asp 55 Phe Thr Lys Val Thr 135	Asn Val Met 40 Gly Ile Asp Glu Ile 120 Asn	Gly Glu 25 Leu Thr Lys Gly Ala 105 Thr	Phe 10 Gly Ala Val Val 90 Ala Ala Asp	Val His Glu Ser 75 Glu Glu Pro Ile Asn	Glu Leu Val 60 Ala Ile Lys Gly Leu 140	Val Leu 45 Lys Glu Val His Gly 125 Asp	Thr 30 Lys Glu Arg Leu 110 Asn	15 Arg Tyr Gly Asp Glu 95 His Asp	Ile Asp Gly Pro 80 Ala Ala Val Glu Met	
178 <211> 179 <212> 180 <213> 181 <400> 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199	LENGTH: TYPE: I ORGANIS SEQUENC Met Val 1 Ala Phe Asn Asp Thr Thi 50 Phe Glu 65 Glu Asn Thr Gly Asn Gly Lys Thi 130	336 PRT SM: S E: 1 Val Arg Leu 35 Gln Val Ile Phe Ala 115 Val	trep 2 Lys Arg 20 Thr Gly Asn Asp Phe 100 Lys Val	Val 5 11e Asp Arg Gly Trp 85 Ala Lys Phe	Gly Gln Pro Phe Asn 70 Ala Lys Val Asn Ala 150	Ile Asn Asn Asp 55 Phe Thr Lys Val Thr 135 Ser	Asn Val Met 40 Gly Ile Asp Glu Ile 120 Asn Cys	Gly Glu 25 Leu Thr Lys Gly Ala 105 Thr His	Phe 10 Gly Ala Val Val 90 Ala Ala Asp	Val His Glu Ser 75 Glu Glu Pro Ile Asn 155	Glu Leu Val 60 Ala Ile Lys Gly Leu 140 Cys	Val Leu 45 Lys Glu Val His Gly 125 Asp Leu	Thr 30 Lys Glu Arg Leu 110 Asn Gly Ala	15 Arg Tyr Gly Asp Glu 95 His Asp Thr	Ile Asp Gly Pro 80 Ala Ala Val Glu Met 160	

RAW SEQUENCE LISTING

DATE: 01/12/2004 TIME: 10:36:11 PATENT APPLICATION: US/10/650,369A

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt Output Set: N:\CRF4\01092004\J650369A.raw

000						1.05					170					175		
203	m	11	T 1 -	114 -	7.1.	165	mb so	C1	7 00	C1 ~		Tlo	T 011	7 00	Clv		uic	
204	1	nr	тте	HIS		Tyr	TIII	СТУ	ASP	185	Mec	TTE	neu	vəħ	190	LIO	1113	
205			~ 1	01	180	T	7	7	71.		חות	ć1	- ות	71.		Tlo	Wal	
. 206	Α	ırg	GIY		Asp	Leu	Arg	Arg		Arg	Ата	GTÀ	Ald		ASII	116	vaı	
207	_		_	195	 \				200	70.7	-1	C1	т	205	т1.	Daga	C3	
208	Р			Ser	Thr	Gly	Ата		ьys	Ата	тте	GTÀ		vaı	тте	PIO	GIU	
209			210		_	_	_	215			-	_	220	_	** . 7	Б	m1	
210			Asn	Gly	Lys	Leu		Gly	Ala	Ala	Gln		vaı	Pro	vaı	Pro		
211		25					230					235	_	_		_	240	
212	G	Пy	Ser	Val	Thr	Glu	Leu	Val	Val	Thr		Asp	Lys	Asn	Val		vai	
213						245				·	250					255		
214	A	Asp	Glu	Ile	Asn	Ala	Ala	Met	Lys	Ala	Ala	Ser	Asn	Asp		Phe	Gly	
215					260					265					270			
216	T	'yr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Val	Ser	Tyr	
217				275					280					285				
218	G	Sly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Met	Glu	Val	Asp	Gly	*
219		_	290					295					300					
220	S	er ·	Gln	Leu	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Met	Ser	Tyr	
221		305				-	310			_	_	315					320	
222			Ala	Gln	Leu	Val	Arq	Thr	Leu	Glu	Tyr	Phe	Ala	Lys	Ile	Ala	Lys	
223 .	_					325					330			-		335	-	
225 <21	0> S	SEO	ו מד	JO: 1	13													
226 <21															•			
227 <21					-													
	ソン・リ																	
=					rant	-000	20118	aga.	lact:	iae								
228 <21	3> 0	RGA	NISN	1: St	rept	tocoo	ccus	aga:	lact	iae								
228 <21 229 <22	3> O 0> F	RGA EAT	NISN URE:	1: St :	-	tocod	ccus	aga:	lacti	iae								
228 <21 229 <22 230 <22	3> 0 0> F 1> N	RGA EAT NAME	NISN URE:	M: St : ۲: CI	os Os			aga:	lacti	iae								
228 <21 229 <22 230 <22 231 <22	3> O 0> F 1> N 2> L	RGA EAT IAME LOCA	NISN URE: KEY	1: St : : CI V: (1	os l)			aga:	lacti	iae								
228 <21 229 <22 230 <22 231 <22 232 <40	3> 0 0> F 1> N 2> L 0> S	ORGA FEAT NAME LOCA SEQU	NISN URE: KEY TION	M: St : Y: CI N: (1 E: 13	- DS L)	(1011	L)	-				aat	cat	ato	aat	cat	ctt	48
228 <21 229 <22 230 <22 231 <22 232 <40 233	3> 0 0> F 1> N 2> L 0> S a	ORGA TEAT NAME LOCA SEQU	NISN URE: KEY TION ENCE gta	M: St : Y: CI N: (1 E: 13 gtt	DS L) B	(101: gtt	l) ggt	att	aac	ggt	ttc	ggt	cgt	atc	ggt	cgt Arg	ctt	48
228 <21 229 <22 230 <22 231 <22 232 <40 233 234	3> 0 0> F 1> N 2> L 0> S a	ORGA FEAT NAME LOCA SEQU Atg	NISN URE: KEY TION ENCE gta	M: St : Y: CI N: (1 E: 13 gtt	DS L) B	(101: gtt Val	l) ggt	att	aac	ggt	Phe	ggt Gly	cgt Arg	atc Ile	ggt Gly	Arg	ctt Leu	48
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235	3> O 0> F 1> N 2> L 0> S a	ORGA FEAT JAME LOCA SEQU Atg Met	NISM URE: /KE) TIOM ENCE gta Val	M: St : Y: CI N: (1 E: 13 gtt Val	OS l) 3 aaa Lys	(1011 gtt Val 5	l) ggt Gly	att Ile	aac Asn	ggt Gly	Phe 10	Gly	Arg	Ile	Gly	Arg 15	Leu	
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236	3> 0 0> F 1> N 2> L 0> S a M	ORGA TEAT NAME LOCA SEQU atg Met 1	NISN URE: KEY TION ENCE gta Val	4: St : :: CI N: (1 E: 13 gtt Val	OS l) 3 aaa Lys	gtt Val 5 atc	l) ggt Gly caa	att Ile	aac Asn gta	ggt Gly gaa	Phe 10 ggt	Gly gtt	Arg gaa	Ile gtt	Gly act	Arg 15 cgt	Leu atc	48 96
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237	3> 0 0> F 1> N 2> L 0> S a M	ORGA TEAT NAME LOCA SEQU atg Met 1	NISN URE: KEY TION ENCE gta Val	4: St : :: CI N: (1 E: 13 gtt Val	DS l) 3 aaa Lys cgc Arg	(1011 gtt Val 5	l) ggt Gly caa	att Ile	aac Asn gta	ggt Gly gaa Glu	Phe 10 ggt	Gly gtt	Arg gaa	Ile gtt	Gly act Thr	Arg 15 cgt	Leu atc	
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238	3> O 0> F 1> N 2> L 0> S a M	ORGA FEAT JAME LOCA SEQU itg Met 1 JCa Ala	NISN URE: KEY TION ENCE gta Val ttc Phe	M: St : Y: CI N: (1 E: 13 gtt Val cgt Arg	DS l) 3 aaa Lys cgc Arg 20	gtt Val 5 atc Ile	ggt Gly caa Gln	att Ile aac Asn	aac Asn gta Val	ggt Gly gaa Glu 25	Phe 10 ggt Gly	Gly gtt Val	Arg gaa Glu	Ile gtt Val	Gly act Thr 30	Arg 15 cgt Arg	Leu atc Ile	96
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239	3> O 0> F 1> N 2> L 0> S a M	DRGA FEAT NAME LOCA SEQU Atg Met 1 JCa Ala	NISM URE: KEY TION ENCE gta Val ttc Phe	4: St : Y: CI N: (1 gtt Val cgt Arg	DS l) aaa Lys cgc Arg 20 aca	gtt Val 5 atc Ile	ggt Gly caa Gln	att Ile aac Asn	aac Asn gta Val atg	ggt Gly gaa Glu 25 ctt	Phe 10 ggt Gly gca	Gly gtt Val cac	Arg gaa Glu ttg	Ile gtt Val ttg	Gly act Thr 30 aaa	Arg 15 cgt Arg tat	Leu atc Ile gac	
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240	3> O 0> F 1> N 2> L 0> S a M	DRGA FEAT NAME LOCA SEQU Atg Met 1 JCa Ala	NISM URE: KEY TION ENCE gta Val ttc Phe	M: St : : : : : : : : : : : : : : : : : : :	DS l) aaa Lys cgc Arg 20 aca	gtt Val 5 atc Ile	ggt Gly caa Gln	att Ile aac Asn	aac Asn gta Val atg Met	ggt Gly gaa Glu 25 ctt	Phe 10 ggt Gly gca	Gly gtt Val cac	Arg gaa Glu ttg	Ile gtt Val ttg Leu	Gly act Thr 30 aaa	Arg 15 cgt Arg tat	Leu atc Ile gac	96
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241	3> O 0> F 1> N 2> L 0> S a M	DRGA TEAT NAME LOCA SEQU Atg Met 1 JCa Ala	NISM URE: /KE) TIOM ENCE gta Val ttc Phe gac Asp	M: St : : : : : : : : : : : : : : : : : : :	DS l) aaa Lys cgc Arg 20 aca Thr	gtt Val 5 atc Ile gat Asp	ggt Gly caa Gln cca Pro	att Ile aac Asn aac Asn	aac Asn gta Val atg Met 40	ggt Gly gaa Glu 25 ctt Leu	Phe 10 ggt Gly gca Ala	Gly gtt Val cac His	Arg gaa Glu ttg Leu	gtt Val ttg Leu 45	Gly act Thr 30 aaa Lys	Arg 15 cgt Arg tat Tyr	atc Ile gac Asp	96 144
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242	3> O 0> F 1> N 2> L 0> S a M g A	DRGA FEAT NAME LOCA SEQU atg Met 1 JCa Ala Mac Asn	NISN FURE: C/KEY TION ENCE gta Val ttc Phe gac Asp	M: St : : : : : : : : : : : : : : : : : : :	DS L) aaaa Lys cgc Arg 20 aca Thr	gtt Val 5 atc Ile gat Asp	ggt Gly caa Gln cca Pro	att Ile aac Asn aac Asn	aac Asn gta Val atg Met 40 ggt	ggt Gly gaa Glu 25 ctt Leu	Phe 10 ggt Gly gca Ala gtt	gtt Val cac His	gaa Glu ttg Leu gtt	gtt Val ttg Leu 45	act Thr 30 aaa Lys	Arg 15 cgt Arg tat Tyr	atc Ile gac Asp	96
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243	3> O 0> F 1> N 2> L 0> S a M g A	DRGA FEAT NAME LOCA SEQU atg Met 1 JCa Ala Mac Asn	NISN FURE: C/KEN TION ENCE gta Val ttc Phe gac Asp act Thr	M: St : : : : : : : : : : : : : : : : : : :	DS L) aaaa Lys cgc Arg 20 aca Thr	gtt Val 5 atc Ile gat Asp	ggt Gly caa Gln cca Pro	att Ile aac Asn aac Asn gac Asp	aac Asn gta Val atg Met 40 ggt	ggt Gly gaa Glu 25 ctt Leu	Phe 10 ggt Gly gca Ala gtt	gtt Val cac His	gaa Glu ttg Leu gtt Val	gtt Val ttg Leu 45	act Thr 30 aaa Lys	Arg 15 cgt Arg tat Tyr	atc Ile gac Asp	96 144
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244	3> O O O > F T O > N O > S A M A A A A A	DRGA FEAT JAME LOCA SEQU Met 1 Jaca Ala Ala Ala Ala Ala Ala	NISN TURE: /KEX TION ENCE gta Val ttc Phe gac Asp act Thr 50	M: St : : CI N: (S E: 13 gtt Val cgt Arg ctt Leu 35 caa Gln	DS l) aaaa Lys cgc Arg 20 aca Thr	gtt Val 5 atc Ile gat Asp cgt	ggt Gly caa Gln cca Pro ttc	att Ile aac Asn aac Asn gac Asp	aac Asn gta Val atg Met 40 ggt Gly	ggt Gly gaa Glu 25 ctt Leu act Thr	Phe 10 ggt Gly gca Ala gtt Val	Gly gtt Val cac His gaa Glu	gaa Glu ttg Leu gtt Val 60	gtt Val ttg Leu 45 aaa Lys	Gly act Thr 30 aaa Lys gaa Glu	Arg 15 cgt Arg tat Tyr ggt Gly	Leu atc Ile gac Asp gga Gly	96 144 192
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245	3> O O O > F T O O > F T O O > S A M A A A A T T T	DRGA FEAT JAME LOCA SEQU Met 1 Jaca Ala Ala Ala Chr	NISN FURE: C/KEN TION ENCE gta Val ttc Phe gac Asp act Thr 50 gaa	M: St : : CI N: (12 St 13 gtt Val cgt Arg ctt Leu 35 caa Gln	DS L) aaaa Lys cgc Arg 20 aca Thr ggt Gly	gtt Val 5 atc Ile gat Asp cgt Arg	ggt Gly caa Gln cca Pro ttc Phe	att Ile aac Asn aac Asn gac Asp 55	aac Asn gta Val atg Met 40 ggt Gly	ggt Gly gaa Glu 25 ctt Leu act Thr	Phe 10 ggt Gly gca Ala gtt Val	Gly gtt Val cac His gaa Glu tct	gaa Glu ttg Leu gtt Val 60 gct	gtt Val ttg Leu 45 aaa Lys	Gly act Thr 30 aaa Lys gaa Glu cgc	Arg 15 cgt Arg tat Tyr ggt Gly	Leu atc Ile gac Asp gga Gly cca	96 144
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245 246	3> O O O > F T O O > F T O O > S A M A A A A T T T	DRGA FEAT JAME LOCA SEQU Met 1 Jaca Ala Ala Ala Chr	NISN FURE: C/KEN TION ENCE gta Val ttc Phe gac Asp act Thr 50 gaa	M: St : : CI N: (12 St 13 gtt Val cgt Arg ctt Leu 35 caa Gln	DS L) aaaa Lys cgc Arg 20 aca Thr ggt Gly	gtt Val 5 atc Ile gat Asp cgt	ggt Gly caa Gln cca Pro ttc Phe caa Gln	att Ile aac Asn aac Asn gac Asp 55	aac Asn gta Val atg Met 40 ggt Gly	ggt Gly gaa Glu 25 ctt Leu act Thr	Phe 10 ggt Gly gca Ala gtt Val	Gly gtt Val cac His gaa Glu tct Ser	gaa Glu ttg Leu gtt Val 60 gct	gtt Val ttg Leu 45 aaa Lys	Gly act Thr 30 aaa Lys gaa Glu cgc	Arg 15 cgt Arg tat Tyr ggt Gly	Leu atc Ile gac Asp gga Gly cca Pro	96 144 192
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245	3> O F F O S O S O S O S O S O S O S O S O	DRGA FEAT NAME LOCA SEQU Met 1 gca Ala Ala Ala Ala Ca Ala Ala Ala Ca Ala Ala Ala Ala Ala Ala Ala Ala Ala Al	NISN FURE: C/KEY TION ENCE gta Val ttc Phe gac Asp act Thr 50 gaa Glu	M: St :: CI N: (SE: 13 gtt Val cgt Arg ctt Leu 35 caa Gln gtt Val	DS l) aaa Lys cgc Arg 20 aca Thr ggt Gly aac	gtt Val 5 atc Ile gat Asp cgt Arg	ggt Gly caa Gln cca Pro ttc Phe caa Gln 70	att Ile aac Asn aac Asn gac Asp 55 ttt Phe	aac Asn gta Val atg Met 40 ggt Gly gtt Val	ggt Gly gaa Glu 25 ctt Leu act Thr	Phe 10 ggt Gly gca Ala gtt Val	Gly gtt Val cac His gaa Glu tct Ser 75	Arg gaa Glu ttg Leu gtt Val 60 gct Ala	gtt Val ttg Leu 45 aaa Lys gaa Glu	Gly act Thr 30 aaa Lys gaa Glu cgc Arg	Arg 15 cgt Arg tat Tyr ggt Gly gaa Glu	Leu atc Ile gac Asp gga Gly cca Pro 80	96 144 192 240
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245 246	3> O F F O S O S O S O S O S O S O S O S O	DRGA FEAT NAME LOCA SEQU Sttg Met 1 JCa Asn Aca Chr ttc 65 JCa	NISN FURE: C/KEY C/K C/K C/K C/K C/K C/K C/K C/K C/K C/K	M: St :: CI M: (SE: 13 gtt Val cgt Arg ctt Leu 35 caa Gln gtt Val	DS l) aaa Lys cgc Arg 20 aca Thr ggt Gly aac Asn	gtt Val 5 atc Ile gat Asp cgt Arg	ggt Gly caa Gln cca Pro ttc Phe caa Gln 70 gct	att Ile aac Asn aac Asn gac Asp 55 ttt Phe act	aac Asn gta Val atg Met 40 ggt Gly gtt Val	ggt Gly gaa Glu 25 ctt Leu act Thr aaa Lys	Phe 10 ggt Gly gca Ala gtt Val gtt Val	Gly gtt Val cac His gaa Glu tct Ser 75 gaa	Arg gaa Glu ttg Leu gtt Val 60 gct Ala atc	gtt Val ttg Leu 45 aaa Lys gaa Glu	Gly act Thr 30 aaa Lys gaa Glu cgc Arg	Arg 15 cgt Arg tat Tyr ggt Gly gaa Glu	Leu atc Ile gac Asp gga Gly cca Pro 80 gca	96 144 192
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247	3> O F F O S O S O S O S O S O S O S O S O	DRGA FEAT NAME LOCA SEQU Sttg Met 1 JCa Asn Aca Chr ttc 65 JCa	NISN FURE: C/KEY C/K C/K C/K C/K C/K C/K C/K C/K C/K C/K	M: St :: CI M: (SE: 13 gtt Val cgt Arg ctt Leu 35 caa Gln gtt Val	DS l) aaa Lys cgc Arg 20 aca Thr ggt Gly aac Asn	gtt Val 5 atc Ile gat Asp cgt Arg	ggt Gly caa Gln cca Pro ttc Phe caa Gln 70 gct	att Ile aac Asn aac Asn gac Asp 55 ttt Phe act	aac Asn gta Val atg Met 40 ggt Gly gtt Val	ggt Gly gaa Glu 25 ctt Leu act Thr aaa Lys	Phe 10 ggt Gly gca Ala gtt Val gtt Val	Gly gtt Val cac His gaa Glu tct Ser 75 gaa	Arg gaa Glu ttg Leu gtt Val 60 gct Ala atc	gtt Val ttg Leu 45 aaa Lys gaa Glu	Gly act Thr 30 aaa Lys gaa Glu cgc Arg	Arg 15 cgt Arg tat Tyr ggt Gly gaa Glu	Leu atc Ile gac Asp gga Gly cca Pro 80 gca	96 144 192 240
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248	3> O F N C S S S S S S S S S S S S S S S S S S	DRGA FEAT UAME LOCA SEQU Atg Ala Ala Asn Aca Fhr ttc Asn Aca Che Asn Aca Asn A	NISN FURE: C/KEY C/K C/K C/K C/K C/K C/K C/K C/K C/K C/K	M: St :: CI V: (SE: 13 gtt Val cgt Arg ctt 35 caa Gln gtt Val	DS l) aaaa Lys cgc Arg 20 aca Thr ggt Gly aac Asn	gtt Val 5 atc Ile gat Asp cgt Arg ggt Gly tgg Trp 85	ggt Gly caa Gln cca Pro ttc Phe caa Gln 70 gct Ala	att Ile aac Asn aac Asn 55 ttt Phe act	aac Asn gta Val atg Met 40 ggt Gly gtt Val gat Asp	ggt Gly gaa Glu 25 ctt Leu act Thr aaa Lys ggc Gly	Phe 10 ggt Gly gca Ala gtt Val gtt Val gta Val 90	Gly gtt Val cac His gaa Glu tct Ser 75 gaa Glu	Arg gaa Glu ttg Leu gtt Val 60 gct Ala atc Ile	gtt Val ttg Leu 45 aaa Lys gaa Glu gtt Val	Gly act Thr 30 aaa Lys gaa Glu cgc Arg ctt Leu	Arg 15 cgt Arg tat Tyr ggt Gly gaa Glu gaa Glu 95	atc Ile gac Asp gga Gly cca Pro 80 gca Ala	96 144 192 240 288
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249	3> OF N L S A A A A A T T T P G A A	DRGA FEAT UAME LOCA SEQU Stg Met 1 JCa Ala Ala Chr Ctc JCa JCa Ala Ala Ct Ala Ala Ct	NISN FURE: C/KEY C/K C/K C/K C/K C/K C/K C/K C/K C/K C/K	M: St :: CI V: (SE: 13 gtt Val cgt Arg ctt 35 cGln gtt Val att Ile	DS l) aaaa Lys cgc Arg 20 aca Thr ggt Gly aac Asn gac Asp	gtt Val 5 atc Ile gat Asp cgt Gly tgg Trp gca	ggt Gly caa Gln cca Pro ttc Phe caa Gln 70 gct Ala	att Ile aac Asn aac Asn gac Asp 55 ttt Phe act Thr	aac Asn gta Val atg Met 40 ggt Val gat Val gat Asp	ggt Gly gaa Glu 25 ctt Leu act Thr aaa Lys ggc Gly	Phe 10 ggt Gly gca Ala gtt Val gta Val gca	Gly gtt Val cac His gaa Glu tct Ser 75 gaa Glu gga	Arg gaa Glu ttg Leu gtt Val 60 gct Ala atc Ile caa	gtt Val ttg Leu 45 aaa Lys gaa Glu gtt Val	Gly act Thr 30 aaa Lys gaa Glu cgc Arg ctt Leu atc	Arg 15 cgt Arg tat Tyr ggt Gly gaa Glu gaa Glu 95 cat	atc Ile gac Asp gga Gly cca Pro 80 gca Ala gaa	96 144 192 240
228 <21 229 <22 230 <22 231 <22 232 <40 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	3> OF N L S A A A A A T T T P G A A	DRGA FEAT UAME LOCA SEQU Stg Met 1 JCa Ala Ala Chr Ctc JCa JCa Ala Ala Ct Ala Ala Ct	NISN FURE: C/KEY C/K C/K C/K C/K C/K C/K C/K C/K C/K C/K	M: St :: CI V: (SE: 13 gtt Val cgt Arg ctt 35 cGln gtt Val att Ile	DS l) aaaa Lys cgc Arg 20 aca Thr ggt Gly aac Asn gac Asp	gtt Val 5 atc Ile gat Asp cgt Arg ggt Gly tgg Trp 85	ggt Gly caa Gln cca Pro ttc Phe caa Gln 70 gct Ala	att Ile aac Asn aac Asn gac Asp 55 ttt Phe act Thr	aac Asn gta Val atg Met 40 ggt Val gat Val gat Asp	ggt Gly gaa Glu 25 ctt Leu act Thr aaa Lys ggc Gly	Phe 10 ggt Gly gca Ala gtt Val gta Val gca	Gly gtt Val cac His gaa Glu tct Ser 75 gaa Glu gga	Arg gaa Glu ttg Leu gtt Val 60 gct Ala atc Ile caa	gtt Val ttg Leu 45 aaa Lys gaa Glu gtt Val	Gly act Thr 30 aaa Lys gaa Glu cgc Arg ctt Leu atc	Arg 15 cgt Arg tat Tyr ggt Gly gaa Glu gaa Glu 95 cat	atc Ile gac Asp gga Gly cca Pro 80 gca Ala gaa	96 144 192 240 288

RAW SEQUENCE LISTING ERROR SUMMARY

PATENT APPLICATION: US/10/650,369A

DATE: 01/12/2004 TIME: 10:36:12

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt Output Set: N:\CRF4\01092004\J650369A.raw

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/650,369A

DATE: 01/12/2004

TIME: 10:36:12

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt Output Set: N:\CRF4\01092004\J650369A.raw

L:716 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:718 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21